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OM protein - protein search, using sw model

Run On: January 16, 2003, 16:39:12, Search time 17.4857 Seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-21

Perfect score: 60

Sequence: 1 ERMRLRIQDYEE 12

Scoring table: BLAST62

Gapop 10 0, Gapext 0 5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 60 | 100 | 0 | 580 | P1976 bos taurus |
| 2 | 60 | 100 | 0 | 585 | P15311 homo sapien |
| 3 | 57 | 95 | 0 | 585 | P26040 mus musculus |
| 4 | 44 | 73.3 | 886 | 1 | O34600 solifolobus |
| 5 | 39 | 65 | 0 | 495 | P12814 homo sapien |
| 6 | 39 | 65 | 0 | 880 | P40048 homo sapien |
| 7 | 38 | 63 | 3 | 715 | P40048 homo sapien |
| 8 | 37 | 61.7 | 303 | 1 | P07751 gallus gall |
| 9 | 37 | 61.7 | 756 | 1 | P07751 gallus gall |
| 10 | 37 | 61.7 | 1005 | 1 | P07751 gallus gall |
| 11 | 37 | 61.7 | 2472 | 1 | P07751 gallus gall |
| 12 | 37 | 61.7 | 2472 | 1 | P07751 gallus gall |
| 13 | 37 | 61.7 | 2472 | 1 | P07751 gallus gall |
| 14 | 36 | 60 | 0 | 320 | P07751 gallus gall |
| 15 | 36 | 60 | 0 | 365 | P07751 gallus gall |
| 16 | 36 | 60 | 0 | 880 | P07751 gallus gall |
| 17 | 36 | 60 | 0 | 892 | P07751 gallus gall |
| 18 | 36 | 60 | 0 | 892 | P07751 gallus gall |
| 19 | 36 | 60 | 0 | 1108 | P07751 gallus gall |
| 20 | 35.5 | 59.2 | 550 | 1 | P07751 gallus gall |
| 21 | 35 | 58.3 | 224 | 1 | P07751 gallus gall |
| 22 | 35 | 58.3 | 519 | 1 | P07751 gallus gall |
| 23 | 35 | 58.3 | 576 | 1 | P07751 gallus gall |
| 24 | 35 | 58.3 | 576 | 1 | P07751 gallus gall |
| 25 | 35 | 58.3 | 583 | 1 | P07751 gallus gall |
| 26 | 35 | 58.3 | 583 | 1 | P07751 gallus gall |
| 27 | 35 | 58.3 | 583 | 1 | P07751 gallus gall |
| 28 | 35 | 58.3 | 721 | 1 | P07751 gallus gall |
| 29 | 35 | 58.3 | 721 | 1 | P07751 gallus gall |
| 30 | 35 | 58.3 | 721 | 1 | P07751 gallus gall |
| 31 | 35 | 58.3 | 891 | 1 | P07751 gallus gall |
| 32 | 35 | 58.3 | 891 | 1 | P07751 gallus gall |
| 33 | 35 | 58.3 | 964 | 1 | P07751 gallus gall |

RESULT 1

1. ERMRL_HOVIN

ID: ERMRL_HOVIN

AC: F31976;

DI: 01-JUL-1993 (Rel. 26, Created)

DT: 01-JUL-1993 (Rel. 26, Last sequence update)

DT: 16 OCT 2001 (Rel. 40, Last annotation update)

DE: ERMRL_HOVIN (Cytovillin) (Villin 2).

GN: Vill2.

OS: Bos taurus (Bovine).

OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC: Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC: Bovidae; Bovinae; Bos.

OX: NCBI_TaxID=9913;

RN: [1]

RP: TISSUE=Brain;

RA: Bergson C.M., Zhao H., Salih K., Duman R.S., Nestler E.J.;

RT: "Ermrl and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus";

RL: Mol. Cell. Neurosci. 4:64-73 (1993).

RN: [2]

RP: TISSUE=Kidney;

RA: MEDLINE=9623137; PubMed=8660651;

RA: Galat A., Garbat M.C., Houet F., Riviere S.;

PT: "Proteins and their amino acid compositions: uniqueness, variability, and applications";

PL: Arch. Biochem. Biophys. 330:229-237 (1996).

CC: -1- FUNCTION: PRE-EXISTING INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.

CC: -2- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN (CYTOSOLASMIC SIDE).

CC: -3- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.

CC: -4- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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CC: ERMRL: M98498; AAA40510, 1; -

CC: InterPro: IPR000299, Band_4.1.

CC: Pfam: PF00379, Ez/rad/moesin.

CC: Pfam: PF00769; ERM; 1.

CC: PRINTS: PR00935; HAND41.

CC: SMART: SM00295; B4.1; 1.

CC: PROSITE: PS00660; BAND_4.1; 1.

CC: PROSITE: PS00661; BAND_4.2; 1.

CC: PROSITE: PS00057; BAND_4.3; 1.

CC: Structural protein, Cytoskeleton; Phosphorylation.

INIT_MET 0 0

ALIGNMENTS

1. ERMRL_HOVIN

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AC: F31976;

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DT: 01-JUL-1993 (Rel. 26, Last sequence update)

DT: 16 OCT 2001 (Rel. 40, Last annotation update)

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GN: Vill2.

OS: Bos taurus (Bovine).

OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC: Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC: Bovidae; Bovinae; Bos.

OX: NCBI_TaxID=9913;

RN: [1]

RP: TISSUE=Brain;

RA: Bergson C.M., Zhao H., Salih K., Duman R.S., Nestler E.J.;

RT: "Ermrl and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus";

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RN: [2]

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RA: MEDLINE=9623137; PubMed=8660651;

RA: Galat A., Garbat M.C., Houet F., Riviere S.;

PT: "Proteins and their amino acid compositions: uniqueness, variability, and applications";

PL: Arch. Biochem. Biophys. 330:229-237 (1996).

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CC: -3- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.

CC: -4- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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CC: ERMRL: M98498; AAA40510, 1; -

CC: InterPro: IPR000299, Band_4.1.

CC: Pfam: PF00379, Ez/rad/moesin.

CC: Pfam: PF00769; ERM; 1.

CC: PRINTS: PR00935; HAND41.

CC: SMART: SM00295; B4.1; 1.

CC: PROSITE: PS00660; BAND_4.1; 1.

CC: PROSITE: PS00661; BAND_4.2; 1.

CC: PROSITE: PS00057; BAND_4.3; 1.

CC: Structural protein, Cytoskeleton; Phosphorylation.

INIT_MET 0 0

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DR EMBL: M65030; AAA92977.1; -
 DR EMBL: M59596; AAA64172.1; -
 DR EMBL: M58597; AAA64173.1; ALT_INIT.
 DR EMBL: S65161; AAB20349.1; -
 DR PIR: A36340; A36340.
 DR Genbank: HGNC:4015; RUT4.
 DR MIM: 104230; -
 DR InterPro: IPR001503; GT_10.
 DR Pfam: PF00852; Glyco_Transf_10; 1
 KW Transferrase; Glycosyltransferase; Transmembrane; Glycoprotein;
 FT Signal-anchor; Gold1 Stack.
 FT DOMAIN 1 22
 FT TRANSMEM 23 47
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT LUMENAL, CATALYTIC (POTENTIAL).
 FT CARBOHYD 91 91
 FT CARBOHYD 190 190
 FT CARBOHYD 190 190
 FT N-LINKED (GLUCNA...) (POTENTIAL).
 FT N-LINKED (GLUCNA...) (POTENTIAL).
 FT CONFLICT 87 87
 FT P -> R (IN REF. 2 AND 3).
 FT CONFLICT 241 241
 FT E -> D (IN REF. 3).
 SQ SEQUENCE 405 AA; 45569 MW; DE72E1FC4902680 CRC64;

Query Match: 65.0%; Score 39; DB 1; Length 405;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FELMLRLQDYEE 12
 II: II: IIII
 Db 136 REVULRVLYEE 147

RESULT 6
 RA50_PYRAB STANDARD; PRI: 880 AA.
 AC QUZCB;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA double-strand break repair rad50 ATPase.
 GN RAD50 OR PAR0812
 OS Pyrococcus abyssi.
 CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 CC Pyrococcus.
 CC NCBI_TaxID=29292;
 CC [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=GP5 / Orsay;
 RA Hollid R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution."
 RL Submitted (JUL1999) to the EMBL/GenBank/DBPFI databases
 CC FUNCTION: Involved in DNA double-strand break repair (DSBP) pho
 CC rad50/mre11 complex possesses single-strand endonuclease activity
 CC and ATP-dependent double-strand-specific exonuclease activity.
 CC Rad50 provides an ATP-dependent control of mre11 by unwinding
 CC and/or repositioning RNA ends into the mre11 active site (By
 CC similarity).
 CC SUBUNIT: Forms a complex with mre11 (By similarity).
 CC SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SURFAMILY.

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DR EMBL: AJ248286; CAB50131.1; -
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ARC_Transport.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 DR ProDom: PD000006; ARC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 DR DNA repair; Hydrolyase; ATP-binding; Coiled coil; Complete proteome.
 FT NP_BIND 30 37
 FT ATP (BY SIMILARITY).
 FT DOMAIN 144 745
 FT COILED COIL (POTENTIAL).
 SQ SEQUENCE 880 AA; 103970 MW; FDI177NC76026479 CRC64;

Query Match: 65.0%; Score 49; DB 1; Length 880;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FELMLRLQDYEE 12
 IIII II: II: II
 Db 589 EELNRLQEELE 600

RESULT 7
 BBS2_HRAHE STANDARD; PRI: 715 AA.
 ID BBS2_HRAHE
 AC Q96SP7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hardet Biedl syndrome 2 protein homolog.
 GN BBS2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-21181710; PubMed 11385252;
 RA Nishimura D.Y.; Searby C.C.; Carmi K.; Elbedour K.; Van Maldergom L.;
 RA Fulton A.H.; Lam B.L.; Powell B.R.; Swiderski R.E.; Huggs K.E.;
 RA Halder N.H.; Wittek-Black A.E.; Ying L.; Duhl D.M.; Gorman S.M.;
 RA Heon E.; Iannaccone A.; Bonneau D.; Biesecker L.G.; Jacobson S.G.;
 RA Stone E.M.; Sheffield V.C.;
 RT "Positional cloning of a novel gene on chromosome 16q causing
 RT Hardet Biedl syndrome (BBS2)."
 RL Hum. Mol. Genet. 10:865-874(2001).

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DR EMBL: AF342739; AAK28555.1; -
 DR SEQUENCE 715 AA; 79125 MW; 326779AC45H36790 CRC64;

Query Match: 63.3%; Score 38; DB 1; Length 715;
 Best Local Similarity 58.3%; Pred. No. 40;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FELMLRLQDYEE 12
 : IIII I: IIII
 Db 346 QNLMLRLNVEE 357

RESULT 8
 CHEV_HACSU STANDARD; PRI: 303 AA.
 ID CHEV_HACSU

RA MEDLINE-21096910; PubMed 11157797;
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
 RA Taratelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Hicks D.K.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.>";
 RL Hum. Mol. Genet. 10:349-352(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wallis J., Lloyd C., Hall R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: Binds to KAP1 and RAD25.
 CC -1- SIMILARITY: CONTAINS 2 EF HAND CALCIUM-BINDING DOMAINS.
 CC
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 CC
 DR EMBL: AF495731; AAL12940.1;
 DR EMBL: AB014565; BAA31640.1;
 DR EMBL: AE006463; AAK61232.1;
 DR EMBL: AL024881; CAB92745.1;
 DR EMBL: AL049542; CAC17519.1;
 DR EMBL: Z98882; CAC17523.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; efhand; 2.
 KW Calcium-binding; Repeat.
 FT CA_BIND 215 225 EF HAND 1 (POTENTIAL).
 FT CA_BIND 247 258 EF HAND 2 (POTENTIAL).
 SQ SEQUENCE 756 AA; 8243 MW; 26431399528AFB9 CRC64;

Query Match 61.7%; Score 37; DB 1; Length 756;
 Best Local Similarity 70.0%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EELMERQDY 10
 III I I I I I
 Db 728 EEINRIQDY 747

RESULT 10
 RA50 MELJA STANDARD; PRI: 1005 AA.
 AC Q58718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA double-strand break repair rad50 Afpase.
 GN RAD50 OR MJ1322.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 UX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-1A1-1 / DSM 2661 / ATCC 43047;
 CC
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake T.A., Finkbeiner S.M., Clayton P.A., Gessyne J.D.,
 RA Kerecavage A.R., Dougherty B.A., Tomb J.P., Adams M.D., Reich C.L.,
 RA Kerlavage A.R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Goodbagen N.S., Weidman T.F., Fuhrmann T.I., Nguyen D.,
 RA Interback T.E., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Burst M.A., Kaine B.P., Berodovsky M.,
 RA Klenk H.P., Fraser C.M., Smith H.G., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanococcal archaeon, Methanococcus
 RA jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The

rad50/mrell complex possesses single-strand endonuclease activity
 and ATP-dependent double-strand-specific exonuclease activity.
 rad50 provides an ATP-dependent control of mrell active site (By
 and/or repositioning DNA ends into the mrell active site (By
 similarity).
 CC -1- SUBUNIT: Forms a complex with mrell (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY, RAD50 SUBFAMILY.
 CC
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 CC
 DR EMBL: U67572; AAR99331.1;
 DR TIGR: M1322;
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 DR Pfam: PF02483; SMC_C; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR DNA repair, Hydrolase, ATP binding; Coiled coil; Complete proteome.
 FT NP_BIND 32 39 ATP (BY SIMILARITY).
 FT DOMAIN 158 849 COILED COIL (POTENTIAL).
 SQ SEQUENCE 1005 AA; 119387 MW; 9888481734788F3 CRC64;
 Query Match 61.7%; Score 37; DB 1; Length 1005;
 Best Local Similarity 58.3%; Pred. No. 66;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EELMERQDYEE 12
 III I I I I I I
 Db 574 EEELKUKYKE 585
 RESULT 11
 SPON_HUMAN STANDARD; PRI: 2472 AA.
 AC Q13813; Q16005; Q9P0V0; Q13186;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
 DE (Alpha 1; spectrin) (Fodrin alpha chain).
 GN SPTAN1 OR SPTA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 UX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-90170946; PubMed-2307671;
 RA Moon R.T., McMahon A.P.;
 RA "Generation of diversity in nonerythroid spectrins. Multiple
 RA polypeptides are predicted by sequence analysis of cDNAs encompassing
 RA the coding region of human nonerythroid alpha-spectrin.";
 RA J. Biol. Chem. 265:4427-4433(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TISSOT fetal brain;
 RA Clanc C.D., Morrow J.S.;
 RA "Complete cDNA sequence of human alpha 11 fetal brain spectrin.";
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 676-1595 FROM N.A.
 CC TISSOT-long;
 CC MEDLINE-88883942; PubMed-2691949;
 RA McMahon A.P., Moon R.T.;
 RA "Structure and evolution of a non-erythroid spectrin, human
 RA alpha-todrin.";

Biochem. Soc. Trans. 15:804-807(1987).
 [4] SEQUENCE OF 676-1595 FROM N.A.
 RX MEDLINE-R7277023; PubMed-3038643;
 RA McMahon A.P., Giebelhaus D.H., Champion J.E., Bailey T.A., Jacey S.,
 RA Carritt B., Henchman S.K., Moon K.T.;
 RT "cDNA cloning, sequencing and chromosome mapping of a non-erythroid
 spectrin, human alpha-fodrin.";
 RL Differentiation 34:68-78(1987)
 [5] ERRATUM.
 RA McMahon A.P., Giebelhaus D.H., Champion J.E., Bailey T.A., Jacey S.,
 RA Carritt B., Henchman S.K., Moon K.T.;
 RL Differentiation 34:241-241(1987).
 [6] SEQUENCE OF 811-1529 FROM N.A. VARIANT ILE-1300, AND MUTAGENESIS
 RC TISSUE-Fetal brain;
 RX MEDLINE-97146462; PubMed-8993318;
 RA Stabach P.F., Glantz S.B., Chang H., Morrow J.S.,
 RT "Site directed mutagenesis of alpha II spectrin at codon 1175
 modulates its mu-calpain susceptibility.";
 RL Biochemistry 36:57-65(1997)
 [7] SEQUENCE OF 1073-1349 FROM N.A.
 RA Murakami N., Speed W.C., Soeman M.I., Zychowski P.L., Wotterberg L.,
 RA Bakstian A.J., Kidd J.P., Kidd K.K.;
 RT "Association and linkage analyses of the non-erythroid alpha-spectrin
 (SPTAN1) gene on chromosome 9q34 with a large Swedish kindred.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
 INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CYTOSKELETON AT THE MEMBRANE
 CC -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 TETRAMERS.
 CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN
 CC -!- SIMILARITY: CONTAINS 23 SPECTRIN REPEATS.
 CC
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 DR FMBL: J05243; AAA51750.1;
 DR EMBL: U83867; AAB41498.1;
 DR EMBL: M24773; AAA52468.1;
 DR EMBL: M18627; AAA51702.1;
 DR EMBL: U26396; AAF60364.1;
 DR EMBL: AF148808; AAF26672.1;
 DR HSSP: P07751; IAFY.
 DR Genew: HGN-11273; SPTAN1.
 DR MIM: 162810.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00036; efhand; 4.
 DR Pfam: PF00435; spectrin; 32.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000012; EF-hand; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00054; EFh; 2.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00150; SPC; 20.
 DR PROSITE: PS00018; EF-HAND; 1.
 DR PROSITE: PS00002; SH3; 1.
 KW Cytoskeleton; Membrane, Calmodulin-binding, Actin-binding;

KW FT REPEAT 10 42 Calcium-binding; Repeat; SH3 domain; Polymorphism.
 FT REPEAT 44 147 SPECTRIN 2.
 FT REPEAT 149 253 SPECTRIN 3.
 FT REPEAT 255 359 SPECTRIN 4.
 FT REPEAT 361 465 SPECTRIN 5.
 FT REPEAT 467 571 SPECTRIN 6.
 FT REPEAT 573 676 SPECTRIN 7.
 FT REPEAT 678 782 SPECTRIN 8.
 FT REPEAT 784 888 SPECTRIN 9.
 FT REPEAT 890 955 SPECTRIN 10.
 FT DOMAIN 967 1026 SH3.
 FT REPEAT 1062 1089 SPECTRIN 11.
 FT REPEAT 1091 1161 SPECTRIN 12.
 FT REPEAT 1208 1231 SPECTRIN 13.
 FT REPEAT 1233 1327 SPECTRIN 14.
 FT REPEAT 1339 1443 SPECTRIN 15.
 FT REPEAT 1445 1549 SPECTRIN 16.
 FT KATA 1551 1656 SPECTRIN 17.
 FT REPEAT 1658 1762 SPECTRIN 18.
 FT REPEAT 1764 1868 SPECTRIN 19.
 FT REPEAT 1870 1974 SPECTRIN 20.
 FT REPEAT 1976 2081 SPECTRIN 21.
 FT REPEAT 2091 2195 SPECTRIN 22.
 FT REPEAT 2205 2310 SPECTRIN 23.
 FT CA-BIND 2336 2347 EF-HAND 1 (POTENTIAL).
 FT SITE 2379 2393 EF-HAND 2 (POTENTIAL).
 FT SITE 1176 1177 CLEAVAGE (BY MU-CALPAIN).
 FT VARIANT 1300 1300 T -> I.
 FT /FTID-VAR-013227.
 FT CONFLICT 150 350 N -> K (IN REF. 2).
 FT CONFLICT 498 498 F -> S (IN REF. 2).
 FT CONFLICT 737 737 V -> I (IN REF. 2).
 FT CONFLICT 1586 1586 Q -> QLSKLL (IN REF. 2).
 FT CONFLICT 1595 1595 F -> P (IN REF. 3 AND 4).
 FT CONFLICT 1625 1625 N -> S (IN REF. 2).
 FT CONFLICT 1670 1671 IA -> FD (IN REF. 2).
 FT CONFLICT 1918 1918 A -> D (IN REF. 2).
 FT CONFLICT 2347 2348 DG -> EF (IN REF. 2).
 FT CONFLICT 2448 2448 I -> Y (IN REF. 2).
 SQ SEQUENCE 2472 AA; 284279 MW; 6241964462A70285 CRC64;
 Query Match 61.7%, Score 37, DB 1, length 2472;
 Best Local Similarity 58.3%; Prod No. 1.8e+02;
 Matches 7, Conservative 3, Mismatches 2, Indels 0, Gaps 0;
 QY 1 EELMLRQDYEE 12
 :|||:|:|:
 DB 969 KRLVLALVDYGE 980
 RESULT 12
 SPCN_RAT ID SPCN_RAT STANDARD; PRT; 2472 AA.
 AC P16086; P70477; Q88663;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non erythroid alpha chain)
 DE (Alpha-II spectrin) (Fodrin alpha chain).
 GN SPTAN1 OR SPTA2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI-TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; ISSUE Liver;
 RA Kalamaraki P., Gazzotti P.;
 RT "Structural and functional characterization of the calmodulin and
 calpain binding domains of rat liver alphaII spectrin.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

anti-parallel triple-helical coiled-coil.";

[7]

RP STRUCTURE BY NMR OF 2320-2403

EX MEDLINE-96067121; PubMed-7588621;

KA Trave G., Jaconbe J. F., Fichtl M., Saraste M., Pastore A.;

RT "Molecular mechanism of the calcium induced conformational change in the spectrin EF-hands";

PL EMBL J. 14:4922-4931(1995);

CC -1- FUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTEINS APPEAR TO BE RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE. THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-BINDING ACTIVITY. IN NONERYTHROID TISSUES, SPECTRINS, IN ASSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORTANT PART IN MEMBRANE ORGANIZATION.

CC -1- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO TETRAMERS.

CC -1- DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:

CC (1) N-TERMINAL DOMAIN (N);

CC (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM);

CC (3) MIDDLE DOMAIN (M);

CC (4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC);

CC (5) C-TERMINAL DOMAIN (C);

CC NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH OTHER. N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT FORM TYPICAL SPECTRIN REPEATS.

CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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DR EMBL: X14518; CAA32462.1; -

DR EMBL: X14519; CAA32463.1; ACT_SEQ.

DR EMBL: X02593; CAA51571.1; ACT_SEQ.

DR PIR: A30122; SJCBA.

DR PDB: 1SHG; 31-OCT-93.

DR PDB: 1AEY; 15-MAY-97.

DR PDB: 1AJ3; 07-JUL-97.

DR PDB: 1TUC; 01-AUG-96.

DR PDB: 1TUD; 01-AUG-96.

DR PDB: 1BK2; 16-FEB-99.

DR InterPro: IPR002048; EF-hand.

DR InterPro: IPR001452; SH3.

DR InterPro: IPR002017; Spectrin

DR Pfam: PF00018; SH3; 1.

DR Pfam: PF00036; cFhand; 2.

DR Pfam: PF00435; spectrin; 23.

DR PRINTS: PR00452; SH3DOMAIN.

DR ProDom: PD000012; EF-hand; 1.

DR ProDom: PD000044; SH3; 1.

DR SMART: SM00054; EFh; 2.

DR SMART: SM00326; SH3; 1.

DR SMART: SM00150; SPM; 20.

DR PROSITE: PS00018; EF-HAND; 2.

DR PROSITE: PS00002; SH3; 1.

KW Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;

KW Capping protein; Calcium-binding; Repeat; SH3 domain; 3D-structure.

FT DOMAIN 1 14 N-TERMINAL DOMAIN.

FT REPEAT 15 119 1.

FT REPEAT 120 225 2.

FT REPEAT 226 331 3.

FT REPEAT 332 437 4.

FT REPEAT 438 543 5.

FT REPEAT 544 648 6.

FT REPEAT 649 754 7.

FT REPEAT 860 966 8.

FT REPEAT 967 1061 9.

FT DOMAIN 1062 1256 MIDDLE DOMAIN.

FT DOMAIN 1062 1256 MC DOMAIN.

FT REPEAT 1257 1362 11.

FT REPEAT 1363 1415 12.

FT REPEAT 1416 1521 13.

FT REPEAT 1522 1633 14.

FT REPEAT 1634 1739 15.

FT REPEAT 1740 1845 16.

FT REPEAT 1846 1951 17.

FT REPEAT 1952 2058 18.

FT REPEAT 2059 2171 19.

FT REPEAT 2172 2256 20.

FT DOMAIN 2257 2477 C-TERMINAL DOMAIN.

FT CA-HIND 2341 2352 EF-HAND 1 (POTENTIAL).

FT CA-HIND 2384 2395 EF-HAND 2 (POTENTIAL).

FT STRAND 971 974

FT STRAND 978 978

FT TURN 983 984

FT STRAND 985 985

FT STRAND 988 988

FT TURN 990 991

FT STRAND 993 998

FT STRAND 1004 1009

FT TURN 1010 1011

FT STRAND 1012 1017

FT HELIX 1018 1020

FT STRAND 1021 1024

SQ SHEET 2477 AA; 24550 MW; A04C876994466A859 DRC64;

Query Match 61.7%; Score 37; DB 1; Length 2477;

Best Local Similarity 56.3%; Pred. No. 1; Re+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HELMRLQDYVE 12

DB 969 KELVLYLDYQE 980

|||||

RESULT 14

ID HLP1_HUMAN STANDARD: PPT: 320 AA.

AC P54257;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE HAP1-like protein 1 (Fragment).

GN HLP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_taxID=9606;

RN 11

RP SEQUENCE FROM N.A.

PC TISSUE=Caudate;

RX MEDLINE-96077112; PubMed-7477378;

RA Li X.-J., Li S.-H., Sharp A.H., Nucleifora F.C. Jr., Schalling G.,

RA Lashan A., Wexley P., Snyder S.H., Ross C.A.;

RT "A huntingtin-associated protein enriched in brain with implications for pathology.";

RL Nature 378:394-402(1995).

CC -1- FUNCTION: IN CONTRAST TO HAP1, DOES NOT SEEM TO BIND TO HUNTINGTIN.

CC -1- SIMILARITY: STRONG, TO HAP1.

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